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Ser Ile Met Thr Asp Leu Tyr Tyr Leu Ser Gln Thr Asp Gly Ala Gly
        35              40              45

Asp Trp Arg Glu Lys Glu Ala Lys Asp Leu Thr Glu Leu Val Gln Arg
    50              55              60

Arg Ile Thr Tyr Leu Gln Asn Pro Lys Asp Cys Ser Lys Ala Lys Lys
 65              70              75              80

Leu Val Cys Asn Ile Asn Lys Gly Cys Gly Tyr Gly Cys Gln Leu His
            85              90              95

His Val Val Tyr Cys Phe Met Ile Ala Tyr Gly Thr Gln Arg Thr Leu
            100             105             110

Ile Leu Glu Ser Gln Asn Trp Arg Tyr Ala Thr Gly Gly Trp Glu Thr
        115             120             125

Val Phe Arg Pro Val Ser Glu Thr Cys Thr Asp Arg Ser Gly Ile Ser
    130             135             140

Thr Gly His Trp Ser Gly Glu Val Lys Asp Lys Asn Val Gln Val Val
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Glu Leu Pro Ile Val Asp Ser Leu His Pro Arg Pro Pro Tyr Leu Pro
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Leu Ala Val Pro Glu Asp Leu Ala Asp Arg Leu Val Arg Val His Gly
                180                    185                    190

Asp Pro Ala Val Trp Trp Val Ser Gln Phe Val Lys Tyr Leu Ile Arg
                195                    200                    205

Pro Gln Pro Trp Leu Glu Lys Glu Ile Glu Glu Ala Thr Lys Lys Leu
    210                    215                    220

Gly Phe Lys His Pro Val Ile Gly Val His Val Arg Arg Thr Asp Lys
225                    230                    235                    240

Val Gly Thr Glu Ala Ala Phe His Pro Ile Glu Glu Tyr Met Val His
                245                    250                    255

Val Glu Glu His Phe Gln Leu Leu Ala Arg Arg Met Gln Val Asp Lys
                260                    265                    270

Lys Arg Val Tyr Leu Ala Thr Asp Asp Pro Ser Leu Leu Lys Glu Ala
                275                    280                    285

Lys Thr Lys Tyr Pro Asn Tyr Glu Phe Ile Ser Asp Asn Ser Ile Ser
    290                    295                    300

Trp Ser Ala Gly Leu His Asn Arg Tyr Thr Glu Asn Ser Leu Arg Gly
305                    310                    315                    320

Val Ile Leu Asp Ile His Phe Leu Ser Gln Ala Asp Phe Leu Val Cys
                325                    330                    335

Thr Phe Ser Ser Gln Val Cys Arg Val Ala Tyr Glu Ile Met Gln Thr
                340                    345                    350

Leu His Pro Asp Ala Ser Ala Asn Phe His Ser Leu Asp Asp Ile Tyr
                355                    360                    365

Tyr Phe Gly Gly Gln Asn Ala His Asn Gln Ile Ala Ile Tyr Ala His

    370                    375                    380

Gln Pro Arg Thr Ala Asp Glu Ile Pro Met Glu Pro Gly Asp Ile Ile
385                    390                    395                    400

Gly Val Ala Gly Asn His Trp Asp Gly Tyr Ser Lys Gly Val Asn Arg
                405                    410                    415

Lys Leu Gly Arg Thr Gly Leu Tyr Pro Ser Tyr Lys Val Arg Glu Lys
                420                    425                    430

Ile Glu Thr Val Lys Tyr Pro Thr Tyr Pro Glu Ala Glu Lys
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Ala Trp Gly Thr Leu Leu Phe Tyr Ile Gly Gly His Leu Val Arg Asp
              20   25   30

Asn Asp His Ser Asp His Ser Ser Arg Glu Leu Ser Lys Ile Leu Ala
          35   40   45

Lys Leu Glu Arg Leu Lys Gln Gln Asn Glu Asp Leu Arg Arg Met Ala
      50   55   60

Glu Ser Leu Arg Ile Pro Glu Gly Pro Ile Asp Gln Gly Pro Ala Ser
 65   70   75   80

Gly Arg Val Arg Ala Leu Glu Glu Gln Phe Met Lys Ala Lys Glu Gln
                  85   90   95

Ile Glu Asn Tyr Lys Lys Gln Thr Lys Asn Gly Pro Gly Lys Asp His
              100   105   110

Glu Ile Leu Arg Arg Arg Ile Glu Asn Gly Ala Lys Glu Leu Trp Phe
          115   120   125

Phe Leu Gln Ser Glu Leu Lys Lys Leu Lys Asn Leu Glu Gly Asn Glu
      130   135   140

Leu Gln Arg His Ala Asp Glu Phe Leu Ser Asp Leu Gly His His Glu
145   150   155   160

Arg Ser Ile Met Thr Asp Leu Tyr Tyr Leu Ser Gln Thr Asp Gly Ala
                  165   170   175

Gly Asp Trp Arg Glu Lys Glu Ala Lys Asp Leu Thr Glu Leu Val Gln
              180   185   190

Arg Arg Ile Thr Tyr Leu Gln Asn Pro Lys Asp Cys Ser Lys Ala Lys
          195   200   205

Lys Leu Val Cys Asn Ile Asn Lys Gly Cys Gly Tyr Gly Cys Gln Leu
      210   215   220

His His Val Val Tyr Cys Phe Met Ile Ala Tyr Gly Thr Gln Arg Thr
225   230   235   240

Leu Ala Leu Glu Ser His Asn Trp Arg Tyr Ala Thr Gly Gly Trp Glu
                  245   250   255

Thr Val Phe Arg Pro Val Ser Glu Thr Cys Thr Asp Arg Ser Gly Ser
                  260   265   270

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Ser Thr Gly His Trp Ser Gly Glu Val Lys Asp Lys Asn Val Gln Val
        275         280             285

Val Glu Leu Pro Ile Val Asp Ser Val His Pro Arg Pro Pro Tyr Leu
    290             295             300

Pro Leu Ala Val Pro Glu Asp Leu Ala Asp Arg Leu Val Arg Val His
305             310             315                     320

Gly Asp Pro Ala Val Trp Trp Val Ser Gln Phe Val Lys Tyr Leu Ile
            325             330                     335

Arg Pro Gln Pro Trp Leu Glu Lys Glu Ile Glu Glu Ala Thr Lys Lys
        340             345             350

Leu Gly Phe Lys His Pro Val Ile Gly Val His Val Arg Arg Thr Asp
        355             360             365

Lys Val Gly Ala Glu Ala Ala Phe His Pro Ile Glu Glu Tyr Thr Val
    370             375             380

His Val Glu Glu Asp Phe Gln Leu Leu Ala Arg Arg Met Gln Val Asp
385             390             395                     400

Lys Lys Arg Val Tyr Leu Ala Thr Asp Asp Pro Ala Leu Leu Lys Glu
            405             410             415

Ala Lys Thr Lys Tyr Pro Ser Tyr Glu Phe Ile Ser Asp Asn Ser Ile
        420             425             430

Ser Trp Ser Ala Gly Leu His Asn Arg Tyr Thr Glu Asn Ser Leu Arg
        435             440             445

Gly Val Ile Leu Asp Ile His Phe Leu Ser Gln Ala Asp Phe Leu Val
    450             455             460

Cys Thr Phe Ser Ser Gln Val Cys Arg Val Ala Tyr Glu Ile Met Gln
465             470             475                     480

Ala Leu His Pro Asp Ala Ser Ala Asn Phe Arg Ser Leu Asp Asp Ile
            485             490             495

Tyr Tyr Phe Gly Gly Pro Asn Ala His Asn Gln Ile Ala Ile Tyr Pro
        500             505             510

His Gln Pro Arg Thr Glu Gly Glu Ile Pro Met Glu Pro Gly Asp Ile
        515             520             525

Ile Gly Val Ala Gly Asn His Trp Asp Gly Tyr Pro Lys Gly Val Asn
    530             535             540

Arg Lys Leu Gly Arg Thr Gly Leu Tyr Pro Ser Tyr Lys Val Arg Glu
545             550             555                     560

Lys Ile Glu Thr Val Lys Tyr Pro Thr Tyr Pro Glu Ala Asp Lys
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<210> 12
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Val Ile Met Ser Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
              20   25   30
ctg tct gca tct cca ggg gag aag gtc aca atg act tgc agg gcc agc   144
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
          35   40   45
tca agt gta agt tac atc cac tgg ttc cag cag aag cca gga tcc tcc   192
Ser Ser Val Ser Tyr Ile His Trp Phe Gln Gln Lys Pro Gly Ser Ser
      50   55   60
ccc aaa ccc tgg att tat gcc aca tcc aac ctg gct tct gga gtc cct   240
Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro
 65   70   75   80
gtt cgc ttc agt ggc agt ggg tct ggg act tct tac tct ctc acc atc   288
Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
              85   90   95
agc aga gtg gag gct gaa gat gct gcc act tat tac tgc cag cag tgg   336
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
             100   105   110
act agt aac cca ccc acg ttc gga ggg ggg acc aag ctg gaa atc aaa   384
Thr Ser Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
         115   120   125

<210> 19
<211> 420
<212> DNA
<213> Mus musculus

<400> 19
atg ggt tgg agc ctc atc ttg ctc ttc ctt gtc gct gtt gct acg cgt   48
Met Gly Trp Ser Leu Ile Leu Leu Phe Leu Val Ala Val Ala Thr Arg
 1   5   10   15
gtc ctg tcc cag gta caa ctg cag cag cct ggg gct gag ctg gtg aag   96
Val Leu Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys

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cct ggg gcc tca gtg aag atg tcc tgc aag gct tct ggc tac aca ttt   144
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
            35                      40                      45
acc agt tac aat atg cac tgg gta aaa cag aca cct ggt cgg ggc ctg   192
Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Arg Gly Leu
    50                      55                      60
gaa tgg att gga gct att tat ccc gga aat ggt gat act tcc tac aat   240
Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn
 65                      70                      75                      80
cag aag ttc aaa ggc aag gcc aca ttg act gca gac aaa tcc tcc agc   288
Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
                    85                      90                      95
aca gcc tac atg cag ctc agc agc ctg aca tct gag gac tct gcg gtc   336
Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
            100                     105                     110
tat tac tgt gca aga tcg act tac tac ggc ggt gac tgg tac ttc aat   384
Tyr Tyr Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn
            115                     120                     125
gtc tgg ggc gca ggg acc acg gtc acc gtc tct gca                   420
Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ala
    130                     135                     140
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<210> 20
<211> 91
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400> 20
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caggaaacag ctatgacgaa ttcgcctcct caaaatggat tttcaggtgc agattatcag 60
cttcctgcta atcagtgctt cagtcataat g                                91
```

<210> 21
<211> 91
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400> 21
```
gtgaccttct cccctggaga tgcagacagg attgctggag actgggagag aacaatttgt 60
cctctggaca ttatgactga agcactgatt a                                91
```

<210> 22
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400> 22
ctccagggga gaaggtcaca atgacttgca gggccagctc aagtgtaagt tacatccact 60
ggttccagca gaagccagga tcctccccca   90

<210> 23
<211> 89
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400> 23
ccagacccac tgccactgaa gcgaacaggg actccagaag ccaggttgga tgtggcataa 60
atccagggtt tgggggagga tcctggctt   89

<210> 24
<211> 91
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400> 24
tcagtggcag tgggtctggg acttcttact ctctcaccat cagcagagtg gaggctgaag 60
atgctgccac ttattactgc cagcagtgga c   91

<210> 25
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400> 25
gttttcccag tcacgaccgt acgtttgatt tccagcttgg tccccctcc gaacgtgggt 60
gggttactag tccactgctg gcagtaataa   90

<210> 26
<211> 99
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400> 26
caggaaacag ctatgacgcg gccgcgaccc ctcaccatgg gttggagcct catcttgctc 60
ttccttgtcg ctgttgctac gcgtgtcctg tcccaggta   99

<210> 27
<211> 98
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400> 27
atgtgtagcc agaagccttg caggacatct tcactgaggc cccagccttc accagctcag 60
ccccaggctg ctgcagttgt acctgggaca ggacacgc   98

<210> 28
<211> 97
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400> 28
caaggcttct ggctacacat ttaccagtta caatatgcac tgggtaaaac agacacctgg 60

tcggggcctg gaatggattg gagctatta tcccgga   97

<210> 29
<211> 99
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400> 29
gtaggctgtg ctggaggatt tgtctgcagt caatgtggcc ttgcctttga acttctgatt 60
gtaggaagta tcaccatttc cgggataaat agctccaat   99

<210> 30
<211> 99
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400> 30
aatcctccag cacagcctac atgcagctca gcagcctgac atctgaggac tctgcggtct 60
attactgtgc aagatcgact tactacggcg gtgactggt   99

<210> 31
<211> 98

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400> 31
gttttcccag tcacgacggg cccttggtgg aggctgcaga gacggtgacc gtggtccctg 60
cgccccagac attgaagtac cagtcaccgc cgtagtaa   98

<210> 32
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400> 32
gagctggtga agcctggggc ctcag   25